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Microbial Communities and Metabolisms From Basalt- and Ultramafic-hosted Vents

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High-temperature vent fields along the Mid-Atlantic Ridge (MAR) are characterized by two different modes of hydrothermal circulation. In basalt-hosted systems fluids rise through gabbros or basaltic lavas, often over long distances along deep-reaching detachment structures. Similar detachments are likely responsible for the formation of hydrothermal fields several kilometres away from the neovolcanic zone in areas of mantle-derived rocks, where the fluids pass through the cooling ultramafic footwall. Consequently, fluid chemical signatures differ considerably according to the host rocks in the subseafloor. The effluents from basalt-hosted settings are generally enriched in sulfide, whereas ultramafic regimes discharge H2 and CH4 enriched fluids. The dilution of the high-temperature endmember solutions with oxygenated ambient seawater also contributes to vent fluid chemistry by admixing oxygen, nitrate and sulfate to the reduced emissions. The fluid-rock interactions and the mixing processes likely denote geochemical constraints on the diversity and activity of local microorganisms.

The hydrothermal fluids of the basalt-hosted vent fields at 5°S and 9°S (Lilliput hydrothermal field) along the MAR are hallmarked by comparatively low H2 concentrations. In contrast, those of the ultramafic-hosted vent fields at 15°N (Logatchev hydrothermal field) and at 8°S (Nibelungen field) along the MAR are considerably enriched in H2. Diffuse and hot hydrothermal effluents from two H2-poor sites in the basalt-hosted southern MAR fields and from four H2-rich localities within the ultramafic-hosted Logatchev field were used for comparing the diversity of H2-oxidizing microbes. To asses the microbial metabolic activities, hydrothermal fluids from seven basalt-hosted vents at 5°S and 9°S and from three ultramafic-host ed sites in the Logatchev and the Nibelungen fields were spiked with H2 or sulfide and supplemented with radioactively labeled inorganic carbon. The fluids were incubated at moderate temperatures and microbial hydrogen or sulfide consumption as well as CO2 fixation rates determined.

The enzyme catalyzing the microbial consumption of H2 is the hydrogenase and its encoding gene is found in phylogenetically diverse microbial lineages. Only few phylogenetically diverging hydrogenase genes were identified in the two H2-poor effluents from the basalt-hosted sites and were associated with those of mesophiles only. On the contrary, a high hydrogenase diversity is illustrated in the four investigated H2-rich Logatchev habitats. Here the hydrogenase genes are affiliated with those of distinct mesophilic and (hyper)thermophilic microbes, reflecting the broad thermal range at which microbial H2-oxidation is putatively performed. The highest microbial H2-consumption rates were exhibited from a basalt-hosted venting sample characterized by extremely low H2 concentrations in the natural

environment (<5 nM) and a very low hydrogenase diversity. In most of the ten fluid incubations H2 could stimulate microbial CO2 fixation, while only in one incubation CO2 fixation could be significantly enhanced by spiking the fluids with sulfide. This indicates the importance of H2 for stimulating microbial CO2 fixation in H2-poor as well as H2-rich vent environments at moderate temperatures. The results also suggest that the availability of H2 in the fluids is not the sole determinant for the diversity and activity of H2-oxidizing microorganisms. Other parameters such as mixing processes influencing the oxygen availability and temperatures of the effluents likely contribute to the metabolic diversity and activity of H2-oxidizing microorganisms in these vent regimes.

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